

Ath 1MDKESFVITQSKAEASPAKQLGVSTVLQLLPSLVKSAQSLARPPPTIS.....KENVAVVGLGSSGRIFLGNNV
 Mes1 1MEQPRFVITAEAEASMAKQSCITVLPOLLPTLVKQARSARLPPTIS.....NMYVGAVGLGSSGRIFGCANL
 Mes2 1MEHPRFVIDASEAESMAKQLGTLVLQLLPTLVKQARSARLPPTIS.....SVYVGAVGLGSSGRIFGCANL
 Lus1 1MEEQVRFVIDAEAEASMTKQGLTRVEGLLPTLVKSAQSLARPPPTIS.....NQVGAVGLGSSGRIFGCANL
 Lus2 1MEEQVRFVIDAEAEASMAKQLGTLKVEELLPTLVKSAQSLARPPPTISNQVGAAGGLGAPPLTRSAISWPRPPTISNQVGAVGLGSSGRIFGCANL
 Ptr1 1MDGPIFVIDASEAESMAKQSCITVLPOLLPTLVKSAQSLARPPPTIS.....KMHVGAVGLGSSGRIFGCANL
 Ptr2 1MDGPIFVIDASEAESMAKQSCITVLPOLLPTLVKSAQSLARPPPTIS.....DMHVGAVGLGSSGRIFGCANL
 Mtr1 1MDREVFVIDAEAEASMAKSSSLTLQLLPSLVKSAQSLARPPPTIS.....NFHVGAVGLGSSGRIFGCANL
 Mtr2 1MEPEKTLIVSEAKSLTQSTNLTLPOLLPTLVKSAQSLARPPPTIS.....KHFVAVAVGISGRIFGVNNV
 Pvul 1 MSRSQIQSTLTLSINNITLLQFPNPMHSP.KTIIIPSEALADASAITLTPOLLPTLVKSAQSLARPPPTIS.....NFVAAVGLGSSGRIFGVNNV
 Pvul2 1MEQAKIKFVIDASEAQSHSS....PIAKLLPSLVKSAQSLARPPPTIS.....NFVAAVGLGSSGRIFGVNNV
 Gma1 1MDPPPSKFVIDASEALALRESAIVTLPELLPTLVKSAQSLARPPPTIS.....KFSVAVGLGSSGRIFGVNNV
 Gma2 1MEPRFVIDASEAESOS.....ISKLLPSLVKSAQSLARPPPTIS.....NFVAAVGLGSSGRIFGVNNV
 Gma3 1MDQPSRKTLIASEALAMAEASAVTLPELLPTLVKSAQSLARPPPTIS.....NFVAAVGLGSSGRIFGVNNV
 Mdo1 1MDREVFVIDASEAESMAKQSNITVLPOLLPSLVKSAQSLARPPPTIS.....KHFVGAVGVGSSGRIFGVNNL
 Mdo2 1MDCPRFVIDASEAESMAKQSNITVLPOLLPSLVKSAQSLARPPPTIS.....KHFVGAVGVGSSGRIFGVNNL
 Bra1 1MDKESFVITPPEAEASPAKQLGVSTVLQLLPSLVNPAKSFARPPPTIS.....KHFVGAVGLGSSGRIFGVNNV
 Bra2 1MDRESLTHAEAEASAAKRRHGVSVVNLLELVLNPAKSLARPPPTIS.....KFPVSAVGLGSSGRIFGVNNV
 Bra3 1MAQPSKFVILNEPYGVSDPMDLVSLIDRRKVLRLMAPIS.....GRHVGAVGLGSSGRIFGVNNV
 Gra1 1MDREVFVIDAEAEAMAKQSKTIVLPOLLPSLVKSAQSLARPPPTIS.....KMHVGAVGLGSSGRIFGCANL
 Gra2 1MDREVFVIDAEAEAMAKQSRQTLVHLLPSLVKSAQSLARPPPTIS.....NMHVGAVGVGSSGRIFGVNNL
 Gra3 1MDPRFVIDAEAEAMAKQSCITVLPOLLPSLVKSAQSLARPPPTIS.....NMHVGAVGVGSSGRIFGVNNL
 Pvi1 1MGEEQVATRPEAAAAPELTGFVMSABAEARAAAAACVATVQDLLELVLVPSAMKRAVVPTIS.....RFVGAVGLGASGRVVGNNL
 Pvi2 1?SABAEARAAAAACVATVQDLLELVLVPSAMNAVVPTIS.....REPRRLGLGASGRVVGNNL

Ath 66 EFPLPLHHSVHAEQFLVTNLNLNGERHLNFFFAVS.....AAPCGHCRQFQEIIRADPDKILITIDPNNS.....ADSDSAADSDGFLRGSLPHRFGPDDLLEKDVPL
 Mes1 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRNAPDKILITIDDSNNNN.....CSGVSONNGDTREESFSRFLPHRFGPDDLLEKDVPL
 Mes2 66 EFPLPLHHSVHAEQFLVTNLNLNAESGLNYAVS.....AAPCGHCRQFQEIIRNAPDKILITIDDSNNNN.....CGGVAENS.GDAKESLSHFLPHRFGPDDLLEKDVPL
 Lus1 66 EFPLPLHHSVHAEQFLVTNLNLNAEPSSMAVS.....SAPCGHCRQFQEIIRSSGSIRLITIDDDHR.....REEDFSRFLPHRFGPDDLLEKDVPL
 Lus2 95 EFPLPLHHSVHAEQFLVTNLNLNAEPAMSSMAVS.....SAPCGHCRQFQEIIRSSGSIRLITIDDDHR.....REEDFSRFLPHRFGPDDLLEKDVPL
 Ptr1 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLKYAVS.....AAPCGHCRQFQEIIRADPDKILITIDGSNSN.....HNYKNDLANEEQEPMSCLPHRFGPDDLLEKDVPL
 Ptr2 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLKYAVS.....AAPCGHCRQFQEIIRADPDKILITIDGSNTNN.....QSYKNDLANEQEPMSCLPHRFGPDDLLEKDVPL
 Mtr1 66 EFPLPLHHSVHAEQFLVTNLNLHDEPNLHFAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....ESDPNFTSLSHFLPHRFGPDDLLEKDVPL
 Mtr2 66 EFPLPLHHSVHAEQFLVTNLNLHDEPNLHFAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....TAKTEFTSLSEFTSLPHRFGPDDLLEKDVPL
 Pvul 92 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....HATPQFTSLSDFLPHRFGPDDLLEKDVPL
 Pvul2 64 EFPLPLHHSVHAEQFLVTNLNLHDEPNLHFAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....HANPNFTSLSHFLPHRFGPDDLLEKDVPL
 Gma1 68 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....EATAEPALSDFLPHRFGPDDLLEKDVPL
 Gma2 59 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....HKNPHEFTSLSHFLPHRFGPDDLLEKDVPL
 Gma3 53 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITIS.....EATAEPALSDFLPHRFGPDDLLEKDVPL
 Mdo1 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITISVESGDD.....NSGLNG.....FDPLHLHLPHRFGPDDLLEKDVPL
 Mdo2 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITISVESGDD.....NSGXNS.....FDPLHLHLPHRFGPDDLLEKDVPL
 Bra1 66 EFPLPLHHSVHAEQFLVTNLNLNGERHLNFFFAVS.....AAPCGHCRQFQEIIRADPDKILITIDPN.....ATADPDADSDGFLRGSLPHRFGPDDLLEKDVPL
 Bra2 66 EFPLPLHHSVHAEQFLVTNLNLNGERHLNFFFAVS.....AAPCGHCRQFQEIIRADPDKILITIDPNADFTVTDKENAVKDENDAVTEKEEDGVREESRFLPHRFGPDDLLEKDVPL
 Bra3 61 EFPLPLHHSVHAEQFLVTNLNLNGERHLNFFFAVS.....AAPCGHCRQFQEIIRADPDKILITIDPNADFTVTDKENAVKDENDAVTEKEEDGVREESRFLPHRFGPDDLLEKDVPL
 Gra1 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITISDESDEKE.....NKISNTCNKDQEPFTSLSHFLPHRFGPDDLLEKDVPL
 Gra2 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITISDESDEKE.....NKISNTCNKDQEPFTSLSHFLPHRFGPDDLLEKDVPL
 Gra3 66 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....AAPCGHCRQFQEIIRADPDKILITISDESDEKE.....NKISNTCNKDQEPFTSLSHFLPHRFGPDDLLEKDVPL
 Pvi1 82 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....HMPCGHCRQFQEIIRADPDKILITIDAEEG.....CAPEPRTASLILRFLPHRFGPDDLLEKDVPL
 Pvi2 58 EFPLPLHHSVHAEQFLVTNLNLNAEPGLNYAVS.....HMPCGHCRQFQEIIRADPDKILITIDAEEG.....CAPEPRTASLILRFLPHRFGPDDLLEKDVPL

Ath 166 LLEPHDNLISDLSDSICNGNT...D.SSALDKQTALAAANKSHAPYSCLPSGVSLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mes1 170 ALEPHNNHLSFVYDSSNSINPGINTP.VCDLKYEAALKKAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mes2 169 ALEPHNNHLSFVYDSSNSINPGINTP.VCDLKYEAALKKAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Lus1 159 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Lus2 187 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Ptr1 168 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Ptr2 168 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mtr1 156 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mtr2 160 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Pvul 182 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Pvul2 154 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gma1 158 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gma2 149 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gma3 143 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mdo1 163 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Mdo2 163 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Bra1 164 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Bra2 180 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Bra3 152 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gra1 170 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gra2 170 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Gra3 170 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Pvi1 176 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT
 Pvi2 152 LLEPHDNLISDLSDSSEGE...K...LKMEEALEAANKSHAPYSCPSGVALLDCEGKVYRGWYMSAAAYNPSLGPVQAALVAVVAGG...GGGYERIVGAVLVEKEDAVVKQDHT

▲ Y in Gma1 derived from genomic sequence

Ath 280 ARLLLETISLPKCEFFVHFHCYEA.....
 Mes1 287 ARLLLOVISLPKCEFFVHFHCYEA.....
 Mes2 286 ARLLLOVISLPKCEFFVHFHCYEA.....
 Lus1 263 ARLLLATVAPKCEFLVHFHCRSG.....
 Lus2 295 ARLLLATVAPKCEFLVHFHCRSG.....
 Ptr1 282 ARLLLKBITSLPKCEFFVHFHCYEA.....
 Ptr2 282 ARLLLKBITSLPKCEFFVHFHCYEA.....
 Mtr1 268 ARLLLEAISLPKCEFLVHFHCYEA.....
 Mtr2 274 ARLLLRISLPKCEFFVHFHCYEA.....
 Pvul 299 ARLLLHSISLPKCEFFVHFHCYEA.....
 Pvul2 262 ARLLLHSISLPKCEFFVHFHCYEA.....
 Gma1 267 ARLLLHSISLPKCEFFVHFHCYEA.....
 Gma2 254 ARLLLHSISLPKCEFFVHFHCYEA.....
 Gma3 251 ARLLLHSISLPKCEFFVHFHCYEA.....
 Mdo1 276 ARLLLOVISLPKCEFFVHFHCYEA.....
 Mdo2 276 ARLLLOVISLPKCEFFVHFHCYEA.....
 Bra1 274 ARLLLOVISLPKCEFFVHFHCYEA.....
 Bra2 289 ARLLLOVISLPKCEFFVHFHCYEA.....
 Bra3 259 ARLLLETISLPKCEFFVHFHCYEA.....
 Gra1 277 ARLLLOVISLPKCEFFVHFHCYEA.....
 Gra2 283 ARLLLOVISLPKCEFFVHFHCYEA.....
 Gra3 282 ARLLLOVISLPKCEFFVHFHCYEA.....
 Pvi1 290 ARLLLOVISLPKCEFFVHFHCYEA.....
 Pvi2 266 ARLLLOVISLPKCEFFVHFHCYEA.....

Supplemental Figure S3. Multiple alignment of CDA from Arabidopsis with CDA protein sequences from several plants possessing more than one CDA gene copy

Most plants with fully sequenced genomes only have a single-copy CDA gene but a few have more than one copy. The corresponding protein sequences were aligned with the CDA from *Arabidopsis* which fully matches the general CDA consensus (Ath). The consensus is derived from Supplemental Figure S1. The alignment was generated with ClustalW and shaded with Boxshade. Additional shading and labelling as in Supplemental Figure S1. Positions diverting from the general CDA consensus (red) and the plant CDA consensus (green triangles) are shaded in yellow. The locus identifiers associated to the aligned sequences are listed in Supplemental Table S2.